

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/574,018
Source: IFWP
Date Processed by STIC: 4/7/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>**> , **EFS Submission User Manual** - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/574,018

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 _____ Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 _____ Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

- 3 ✓ _____ Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

- 4 _____ Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

- 5 _____ Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 _____ PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

- 7 _____ Skipped Sequences
 (OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped
 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

- 8 _____ Skipped Sequences
 (NEW RULES) Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

- 9 _____ Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
 In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

- 10 ✓ _____ Invalid <213>
 Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

- 11 _____ Use of <220> Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules

- 12 _____ PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

- 13 _____ Misuse of n/Xaa "**n**" can **only** represent a single nucleotide; "**Xaa**" can **only** represent a single amino acid



IFWP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/574,018

DATE: 04/07/2006

TIME: 11:04:48

Input Set : A:\pto.da.txt

Output Set: N:\CRF4\04072006\J574018.raw

3 <110> APPLICANT: The Hospital for Sick Children
 5 <120> TITLE OF INVENTION: Method of in situ Detection of Proteins Using
 6 Aptamers
 8 <130> FILE REFERENCE: 3206-276 LAB
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/574,018
 C--> 10 <141> CURRENT FILING DATE: 2006-03-29
 10 <150> PRIOR APPLICATION NUMBER: U.S. 60/506776
 11 <151> PRIOR FILING DATE: 2003-09-30
 13 <150> PRIOR APPLICATION NUMBER: PCT/CA2004/001757
 14 <151> PRIOR FILING DATE: 2004-09-29
 16 <160> NUMBER OF SEQ ID NOS: 9
 18 <170> SOFTWARE: PatentIn Ver. 3.1

ERRORED SEQUENCES

49 <210> SEQ ID NO: 3
 50 <211> LENGTH: 12
 51 <212> TYPE: PRT
 52 <213> ORGANISM: Peptide (see item 10 on Error summary sheet)
 54 <400> SEQUENCE: 3
 56 Met Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly
 E--> 57 1 5 10 misaligned numbering (see item 3 on Error summary sheet)
 60 <210> SEQ ID NO: 4
 61 <211> LENGTH: 73
 62 <212> TYPE: DNA
 63 <213> ORGANISM: Artificial
 65 <220> FEATURE:
 66 <223> OTHER INFORMATION: Primer
 68 <400> SEQUENCE: 4
 W--> 70 ggggttttaag cttaccatgg gatatcccta tgatgtgccca gactacgagg gaatgtctag 60
 E--> 71 agt 73
 128 <210> SEQ ID NO: 9
 129 <211> LENGTH: 41
 130 <212> TYPE: DNA
 131 <213> ORGANISM: Artificial
 133 <220> FEATURE:
 134 <223> OTHER INFORMATION: Primer
 136 <400> SEQUENCE: 9
 138 ggcgacatac gttctctatc actgataggg agtaaactcg t
 E--> 141 2 - delete
 41
 attagataaa
 insert a hard return
 move these to next line
 Per 1.822 of sequence Rules
 a maximum of 60 nucleotides per line

RAW SEQUENCE LISTING ERROR SUMMARY
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FYI

Input Set : A:\pto.da.txt
Output Set: N:\CRF4\04072006\J574018.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:4; Line(s) 70

Invalid <213> Response:

ignore
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,4,5,6,7,8,9

VERIFICATION SUMMARY

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Input Set : A:\pto.da.txt

Output Set: N:\CRF4\04072006\J574018.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:57 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:70 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:8
L:71 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:71 M:254 E: No. of Bases conflict, LENGTH:Input:73 Counted:3 SEQ:4
L:71 M:252 E: No. of Seq. differs, <211> LENGTH:Input:73 Found:3 SEQ:4
L:141 M:254 E: No. of Bases conflict, this line has no nucleotides.